GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 914 Seconds
                                            (without alignments)
                                            297.960 Million cell updates/sec

Title: US-10-529-447-24
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
        1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
        2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
        3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
        4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
        5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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       21:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq8:*
       22:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	26	8	US-10-529-447-23	Sequence 23, Appl
2	26	100.0	26	8	US-10-529-447-24	Sequence 24, Appl
3	26	100.0	7857	11	US-10-959-175-2	Sequence 2, Appli
4	24.4	93.8	1000	14	US-11-266-748A-392280	Sequence 392280,
c 5	24.4	93.8	1000	14	US-11-266-748A-482998	Sequence 482998,
6	20.2	77.7	7896	11	US-10-528-311-4	Sequence 4, Appli
c 7	19.6	75.4	503	18	US-11-241-607-66124	Sequence 66124, A
c 8	19.6	75.4	503	18	US-11-241-607-66124	Sequence 66124, A
c 9	19.6	75.4	586	20	US-11-503-243A-7736	Sequence 7736, Ap
c 10	19.6	75.4	729	14	US-11-216-545-5525	Sequence 5525, Ap
c 11	19.6	75.4	1239	8	US-10-863-905-320	Sequence 320, App
c 12	19.6	75.4	73634	8	US-10-035-832-1133	Sequence 1133, Ap
c 13	19.6	75.4	73634	16	US-11-330-726-121	Sequence 121, App
14	19.2	73.8	430	12	US-10-703-032-85228	Sequence 85228, A
15	18.8	72.3	939	14	US-11-217-529-80024	Sequence 80024, A
16	18.8	72.3	1013	10	US-10-750-622-57195	Sequence 57195, A
17	18.8	72.3	1090936	9	US-10-915-727-12210	Sequence 12210, A
18	18.6	71.5	201	6	US-10-990-328-512707	Sequence 512707,
19	18.6	71.5	402	21	US-11-497-489A-25273	Sequence 25273, A
20	18.6	71.5	421	21	US-11-497-489A-236110	Sequence 236110,
21	18.6	71.5	586	21	US-11-443-428A-419553	Sequence 419553,
22	18.6	71.5	1983	21	US-11-443-428A-419524	Sequence 419524,
23	18.6	71.5	7808	11	US-10-959-175-4	Sequence 4, Appli
24	18.6	71.5	33494	18	US-11-491-125A-49957	Sequence 49957, A
c 25	18.6	71.5	37621	5	US-09-815-264-80619	Sequence 80619, A
c 26	18.6	71.5	37621	13	US-11-595-983-80619	Sequence 80619, A
c 27	18.6	71.5	92861	11	US-10-540-898-820	Sequence 820, App
28	18.6	71.5	1980090	6	US-10-990-328-97595	Sequence 97595, A
c 29	18.2	70.0	32	11	US-10-536-560-412547	Sequence 412547,
30	18.2	70.0	435	11	US-10-501-933-489	Sequence 489, App
31	18.2	70.0	635	5	US-09-815-264-84241	Sequence 84241, A
32	18.2	70.0	635	13	US-11-595-983-84241	Sequence 84241, A
c 33	18.2	70.0	700	20	US-11-433-832-35650	Sequence 35650, A
34	18.2	70.0	921	21	US-11-443-428A-663869	Sequence 663869,
c 35	18.2	70.0	1000	14	US-11-266-748A-221988	Sequence 221988,
c 36	18.2	70.0	1595	20	US-11-433-832-45324	Sequence 45324, A
c 37	18.2	70.0	1739	11	US-10-219-051B-11337	Sequence 11337, A
c 38	18.2	70.0	1800	14	US-11-266-748A-31771	Sequence 31771, A
c 39	18.2	70.0	1954	21	US-11-443-428A-324149	Sequence 324149,
c 40	18.2	70.0	2009	21	US-11-443-428A-324157	Sequence 324157,
c 41	18.2	70.0	2040	21	US-11-443-428A-324150	Sequence 324150,
c 42	18.2	70.0	2285	21	US-11-443-428A-324156	Sequence 324156,
c 43	18.2	70.0	2524	21	US-11-443-428A-324151	Sequence 324151,
c 44	18.2	70.0	6972	7	US-10-940-774-13195	Sequence 13195, A
45	18.2	70.0	8140	5	US-09-815-264-69722	Sequence 69722, A

ALIGNMENTS

RESULT 1
US-10-529-447-23

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 914 Seconds
                                    (without alignments)
                                    297.960 Million cell updates/sec

Title: US-10-529-447-23
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
        1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
        2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
        3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
        4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
        5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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SUMMARIES

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c 9	19.6	75.4	586	20	US-11-503-243A-7736	Sequence 7736, Ap
c 10	19.6	75.4	729	14	US-11-216-545-5525	Sequence 5525, Ap
c 11	19.6	75.4	1239	8	US-10-863-905-320	Sequence 320, App
c 12	19.6	75.4	73634	8	US-10-035-832-1133	Sequence 1133, Ap
c 13	19.6	75.4	73634	16	US-11-330-726-121	Sequence 121, App
14	19.2	73.8	430	12	US-10-703-032-85228	Sequence 85228, A
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c 27	18.6	71.5	92861	11	US-10-540-898-820	Sequence 820, App
28	18.6	71.5	1980090	6	US-10-990-328-97595	Sequence 97595, A
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32	18.2	70.0	635	13	US-11-595-983-84241	Sequence 84241, A
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c 35	18.2	70.0	1000	14	US-11-266-748A-221988	Sequence 221988,
c 36	18.2	70.0	1595	20	US-11-433-832-45324	Sequence 45324, A
c 37	18.2	70.0	1739	11	US-10-219-051B-11337	Sequence 11337, A
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c 43	18.2	70.0	2524	21	US-11-443-428A-324151	Sequence 324151,
c 44	18.2	70.0	6972	7	US-10-940-774-13195	Sequence 13195, A
45	18.2	70.0	8140	5	US-09-815-264-69722	Sequence 69722, A

ALIGNMENTS

RESULT 1
US-10-529-447-23

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 809 Seconds
                                          (without alignments)
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Title: US-10-529-447-22
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                 3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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                 22: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
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SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	23	100.0	23	8	US-10-529-447-22	Sequence 22, Appl
c	2	18.2	79.1	10381	18	US-11-491-125A-65888	Sequence 65888, A
c	3	18.2	79.1	15607	18	US-11-491-125A-47929	Sequence 47929, A
c	4	18.2	79.1	46292	5	US-09-815-264-75225	Sequence 75225, A
c	5	18.2	79.1	46292	13	US-11-595-983-75225	Sequence 75225, A
	6	17.8	77.4	367	20	US-11-503-243A-331545	Sequence 331545,
	7	17.8	77.4	389	11	US-10-612-783-2957	Sequence 2957, Ap
	8	17.4	75.7	29871	10	US-10-803-180-1694	Sequence 1694, Ap
	9	17.4	75.7	29871	20	US-11-066-316A-9865	Sequence 9865, Ap
c	10	17.4	75.7	312957	8	US-10-893-319-31	Sequence 31, Appl
c	11	17.4	75.7	312972	8	US-10-893-319-34	Sequence 34, Appl
c	12	17.4	75.7	321019	10	US-10-803-180-1664	Sequence 1664, Ap
c	13	17.4	75.7	321019	20	US-11-066-316A-9851	Sequence 9851, Ap
	14	17.2	74.8	304	6	US-10-205-189A-6401	Sequence 6401, Ap
	15	17.2	74.8	315	20	US-11-503-243A-138083	Sequence 138083,
	16	17.2	74.8	410	21	US-11-497-489A-225161	Sequence 225161,
	17	17.2	74.8	488	13	US-11-486-299A-57998	Sequence 57998, A
	18	17.2	74.8	500	21	US-11-497-489A-72196	Sequence 72196, A
c	19	17.2	74.8	596	21	US-11-497-489A-44327	Sequence 44327, A
	20	17.2	74.8	1027	5	US-09-815-264-57750	Sequence 57750, A
	21	17.2	74.8	1027	13	US-11-595-983-57750	Sequence 57750, A
	22	17.2	74.8	1027	18	US-11-491-125A-48199	Sequence 48199, A
	23	17.2	74.8	1113	13	US-11-635-706-3370	Sequence 3370, Ap
	24	17.2	74.8	1856	20	US-11-503-243A-272053	Sequence 272053,
	25	17.2	74.8	2013	15	US-11-218-305-10034	Sequence 10034, A
	26	17.2	74.8	2262	20	US-11-253-199-1200	Sequence 1200, Ap
	27	17.2	74.8	2435	11	US-10-449-902-17517	Sequence 17517, A
	28	17.2	74.8	8242	5	US-09-815-264-62890	Sequence 62890, A
	29	17.2	74.8	8242	13	US-11-595-983-62890	Sequence 62890, A
	30	17.2	74.8	8242	18	US-11-491-125A-53306	Sequence 53306, A
	31	17.2	74.8	21048	5	US-09-815-264-68782	Sequence 68782, A
	32	17.2	74.8	21048	13	US-11-595-983-68782	Sequence 68782, A
	33	17.2	74.8	21048	18	US-11-491-125A-55219	Sequence 55219, A
c	34	17.2	74.8	26558	5	US-09-815-264-68767	Sequence 68767, A
c	35	17.2	74.8	26558	13	US-11-595-983-68767	Sequence 68767, A
c	36	17.2	74.8	26860	18	US-11-491-125A-39177	Sequence 39177, A
	37	17.2	74.8	210383	6	US-10-990-328-94143	Sequence 94143, A
c	38	17	73.9	954	21	US-11-443-428A-519462	Sequence 519462,
	39	16.8	73.0	425	21	US-11-497-489A-212043	Sequence 212043,
	40	16.8	73.0	546	20	US-11-503-243A-437071	Sequence 437071,
c	41	16.8	73.0	881	20	US-11-503-243A-273813	Sequence 273813,
c	42	16.8	73.0	2390	15	US-11-218-305-17094	Sequence 17094, A
c	43	16.8	73.0	2471	15	US-11-218-305-17093	Sequence 17093, A
c	44	16.8	73.0	2697	11	US-10-449-902-16450	Sequence 16450, A
c	45	16.8	73.0	20578	5	US-09-815-264-64441	Sequence 64441, A

ALIGNMENTS

RESULT 1
US-10-529-447-22

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 773 Seconds
                                            (without alignments)
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Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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        22: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	8	US-10-529-447-8	Sequence 8, Appli
c	2	22	100.0	1000	14	US-11-266-748A-392280	Sequence 392280,
	3	22	100.0	1000	14	US-11-266-748A-482998	Sequence 482998,
	4	18.8	85.5	3002	10	US-10-750-622-33459	Sequence 33459, A
	5	18.4	83.6	1497	14	US-11-216-545-2700	Sequence 2700, Ap
c	6	17.8	80.9	2380	21	US-11-443-428A-596879	Sequence 596879,
c	7	17.8	80.9	2561	21	US-11-443-428A-596883	Sequence 596883,
	8	17.8	80.9	6787	21	US-11-043-591-335	Sequence 335, App
	9	17.8	80.9	6800	21	US-11-043-591-337	Sequence 337, App
	10	17.8	80.9	6801	11	US-10-219-051B-7964	Sequence 7964, Ap
	11	17.8	80.9	6801	11	US-10-219-051B-7968	Sequence 7968, Ap
	12	17.8	80.9	6809	21	US-11-043-591-340	Sequence 340, App
	13	17.8	80.9	6859	21	US-11-043-591-338	Sequence 338, App
	14	17.8	80.9	6898	21	US-11-043-591-336	Sequence 336, App
	15	17.8	80.9	6924	21	US-11-043-591-339	Sequence 339, App
	16	17.8	80.9	7232	21	US-11-443-428A-300721	Sequence 300721,
	17	17.8	80.9	7851	11	US-10-219-051B-8037	Sequence 8037, Ap
c	18	17.8	80.9	7857	11	US-10-959-175-2	Sequence 2, Appli
	19	17.8	80.9	7941	11	US-10-219-051B-7966	Sequence 7966, Ap
	20	17.8	80.9	7941	11	US-10-219-051B-7970	Sequence 7970, Ap
	21	17.8	80.9	7941	11	US-10-219-051B-8039	Sequence 8039, Ap
	22	17.8	80.9	7941	12	US-10-245-882-367	Sequence 367, App
	23	17.8	80.9	7941	15	US-11-226-554-32	Sequence 32, Appl
	24	17.8	80.9	7941	15	US-11-248-718-32	Sequence 32, Appl
	25	17.8	80.9	7941	20	US-11-538-552-32	Sequence 32, Appl
	26	17.8	80.9	7941	21	US-11-043-591-465	Sequence 465, App
	27	17.8	80.9	7994	21	US-11-443-428A-300723	Sequence 300723,
	28	17.8	80.9	8034	21	US-11-443-428A-300719	Sequence 300719,
	29	17.8	80.9	8048	6	US-10-990-328-6021	Sequence 6021, Ap
	30	17.8	80.9	8048	10	US-10-796-280-544	Sequence 544, App
	31	17.8	80.9	8070	21	US-11-443-428A-300720	Sequence 300720,
	32	17.8	80.9	8091	21	US-11-443-428A-300718	Sequence 300718,
	33	17.8	80.9	8136	6	US-10-990-328-6024	Sequence 6024, Ap
	34	17.8	80.9	8136	10	US-10-796-280-547	Sequence 547, App
	35	17.8	80.9	8169	13	US-11-582-861-12059	Sequence 12059, A
	36	17.8	80.9	8208	21	US-11-443-428A-300722	Sequence 300722,
	37	17.8	80.9	8266	6	US-10-990-328-6023	Sequence 6023, Ap
	38	17.8	80.9	8266	10	US-10-796-280-546	Sequence 546, App
	39	17.8	80.9	54461	7	US-10-940-774-16411	Sequence 16411, A
	40	17.8	80.9	56700	8	US-10-940-774-12573	Sequence 12573, A
	41	17.8	80.9	65424	6	US-10-990-328-95881	Sequence 95881, A
	42	17.8	80.9	201037	6	US-10-990-328-95609	Sequence 95609, A
	43	17.8	80.9	201037	10	US-10-796-280-12373	Sequence 12373, A
c	44	17.4	79.1	601	7	US-10-940-774-70106	Sequence 70106, A
c	45	17.4	79.1	601	7	US-10-940-774-70107	Sequence 70107, A

ALIGNMENTS

RESULT 1
US-10-529-447-8

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 738 Seconds
                                            (without alignments)
                                            297.960 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	8	US-10-529-447-7	Sequence 7, Appli
c	2	21	100.0	2380	21	US-11-443-428A-596879	Sequence 596879,
c	3	21	100.0	2561	21	US-11-443-428A-596883	Sequence 596883,
c	4	21	100.0	7857	11	US-10-959-175-2	Sequence 2, Appli
	5	18.4	87.6	450	21	US-11-497-489A-34572	Sequence 34572, A
c	6	17.4	82.9	1555	10	US-10-750-622-44225	Sequence 44225, A
c	7	16.8	80.0	201	6	US-10-990-328-547399	Sequence 547399,
	8	16.8	80.0	452	12	US-10-703-032-42891	Sequence 42891, A
c	9	16.8	80.0	601	7	US-10-940-774-178768	Sequence 178768,
	10	16.8	80.0	824	14	US-11-266-748A-9321	Sequence 9321, Ap
c	11	16.8	80.0	824	14	US-11-266-748A-64033	Sequence 64033, A
	12	16.8	80.0	824	14	US-11-266-748A-66865	Sequence 66865, A
	13	16.8	80.0	824	14	US-11-266-748A-171084	Sequence 171084,
c	14	16.8	80.0	824	14	US-11-266-748A-245254	Sequence 245254,
	15	16.8	80.0	935	21	US-11-443-428A-196716	Sequence 196716,
	16	16.8	80.0	979	14	US-11-266-748A-255874	Sequence 255874,
c	17	16.8	80.0	979	14	US-11-266-748A-316391	Sequence 316391,
	18	16.8	80.0	1262	14	US-11-266-748A-98000	Sequence 98000, A
c	19	16.8	80.0	1262	14	US-11-266-748A-150811	Sequence 150811,
c	20	16.8	80.0	1425	15	US-11-348-413-11105	Sequence 11105, A
c	21	16.8	80.0	1437	8	US-10-902-441-2228	Sequence 2228, Ap
c	22	16.8	80.0	1437	18	US-11-207-802-2228	Sequence 2228, Ap
c	23	16.8	80.0	1437	20	US-11-208-208-2228	Sequence 2228, Ap
c	24	16.8	80.0	1935	14	US-11-293-697-100	Sequence 100, App
	25	16.8	80.0	1963	11	US-10-760-320A-2086	Sequence 2086, Ap
	26	16.8	80.0	1983	21	US-11-443-428A-259366	Sequence 259366,
c	27	16.8	80.0	5386	6	US-10-777-288A-1747	Sequence 1747, Ap
c	28	16.8	80.0	6585	14	US-11-266-748A-22534	Sequence 22534, A
c	29	16.8	80.0	6925	14	US-11-266-748A-32263	Sequence 32263, A
c	30	16.8	80.0	7170	21	US-11-443-428A-463748	Sequence 463748,
c	31	16.8	80.0	7400	21	US-11-443-428A-463747	Sequence 463747,
c	32	16.8	80.0	7567	21	US-11-443-428A-463741	Sequence 463741,
c	33	16.8	80.0	7610	14	US-11-266-748A-28550	Sequence 28550, A
c	34	16.8	80.0	7644	14	US-11-266-748A-56314	Sequence 56314, A
c	35	16.8	80.0	8139	21	US-11-443-428A-463738	Sequence 463738,
c	36	16.8	80.0	8359	21	US-11-443-428A-463740	Sequence 463740,
c	37	16.8	80.0	8551	21	US-11-443-428A-463749	Sequence 463749,
	38	16.8	80.0	10733	7	US-10-940-774-16876	Sequence 16876, A
c	39	16.8	80.0	168751	6	US-10-990-328-98075	Sequence 98075, A
	40	16.8	80.0	273853	6	US-10-990-328-98181	Sequence 98181, A
	41	16.4	78.1	290	21	US-11-443-428A-98435	Sequence 98435, A
c	42	16.4	78.1	341	21	US-11-443-428A-706911	Sequence 706911,
	43	16.4	78.1	1899	18	US-11-491-125A-39722	Sequence 39722, A
c	44	16.4	78.1	3257	18	US-11-491-125A-44048	Sequence 44048, A
	45	16.4	78.1	4335	18	US-11-491-125A-44318	Sequence 44318, A

ALIGNMENTS

RESULT 1
US-10-529-447-7

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 738 Seconds
                                           (without alignments)
                                           297.960 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
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Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	8	US-10-529-447-5	Sequence 5, Appli
2	21	100.0	21	8	US-10-529-447-6	Sequence 6, Appli
3	21	100.0	2380	21	US-11-443-428A-596879	Sequence 596879,
4	21	100.0	2561	21	US-11-443-428A-596883	Sequence 596883,
5	21	100.0	7857	11	US-10-959-175-2	Sequence 2, Appli
6	18	85.7	1000	14	US-11-266-748A-392280	Sequence 392280,
c 7	18	85.7	1000	14	US-11-266-748A-482998	Sequence 482998,
8	17.8	84.8	453	14	US-11-266-748A-103667	Sequence 103667,
c 9	17.8	84.8	453	14	US-11-266-748A-156478	Sequence 156478,
10	17.8	84.8	463	21	US-11-443-428A-160893	Sequence 160893,
11	17.8	84.8	1120	14	US-11-266-748A-73083	Sequence 73083, A
c 12	17.8	84.8	1120	14	US-11-266-748A-125894	Sequence 125894,
13	17.8	84.8	7896	11	US-10-528-311-4	Sequence 4, Appli
c 14	17.8	84.8	86592	11	US-10-497-268-1	Sequence 1, Appli
15	17.4	82.9	2000	10	US-10-750-622-33522	Sequence 33522, A
16	16.8	80.0	201	6	US-10-990-328-118786	Sequence 118786,
c 17	16.8	80.0	240	21	US-11-497-489A-51738	Sequence 51738, A
18	16.8	80.0	398	21	US-11-497-489A-28993	Sequence 28993, A
c 19	16.8	80.0	488	14	US-11-266-748A-178608	Sequence 178608,
20	16.8	80.0	488	14	US-11-266-748A-246340	Sequence 246340,
c 21	16.8	80.0	488	14	US-11-266-748A-263857	Sequence 263857,
22	16.8	80.0	488	14	US-11-266-748A-324374	Sequence 324374,
23	16.8	80.0	494	21	US-11-443-428A-409401	Sequence 409401,
c 24	16.8	80.0	619	14	US-11-266-748A-5478	Sequence 5478, Ap
c 25	16.8	80.0	657	21	US-11-443-428A-123464	Sequence 123464,
c 26	16.8	80.0	676	14	US-11-266-748A-359762	Sequence 359762,
27	16.8	80.0	676	14	US-11-266-748A-443141	Sequence 443141,
28	16.8	80.0	898	21	US-11-443-428A-72587	Sequence 72587, A
c 29	16.8	80.0	1076	14	US-11-266-748A-79710	Sequence 79710, A
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c 33	16.8	80.0	1932	15	US-11-056-355B-93681	Sequence 93681, A
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c 35	16.8	80.0	3956	14	US-11-266-748A-24661	Sequence 24661, A
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c 37	16.8	80.0	4025	21	US-11-443-428A-123461	Sequence 123461,
c 38	16.8	80.0	4389	21	US-11-443-428A-123463	Sequence 123463,
39	16.8	80.0	4789	14	US-11-266-748A-27829	Sequence 27829, A
c 40	16.8	80.0	12858	6	US-10-990-328-96819	Sequence 96819, A
41	16.8	80.0	35218	6	US-10-990-328-93486	Sequence 93486, A
42	16.8	80.0	49186	10	US-10-796-280-12576	Sequence 12576, A
43	16.8	80.0	56319	10	US-10-767-471-10618	Sequence 10618, A
44	16.8	80.0	56324	20	US-11-066-316A-9912	Sequence 9912, Ap
45	16.8	80.0	129336	6	US-10-990-328-97125	Sequence 97125, A

ALIGNMENTS

RESULT 1
US-10-529-447-5

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 738 Seconds
                                          (without alignments)
                                          297.960 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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                 2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	8	US-10-529-447-5	Sequence 5, Appli
	2	21	100.0	21	8	US-10-529-447-6	Sequence 6, Appli
	3	21	100.0	2380	21	US-11-443-428A-596879	Sequence 596879,
	4	21	100.0	2561	21	US-11-443-428A-596883	Sequence 596883,
	5	21	100.0	7857	11	US-10-959-175-2	Sequence 2, Appli
	6	18	85.7	1000	14	US-11-266-748A-392280	Sequence 392280,
c	7	18	85.7	1000	14	US-11-266-748A-482998	Sequence 482998,
	8	17.8	84.8	453	14	US-11-266-748A-103667	Sequence 103667,
c	9	17.8	84.8	453	14	US-11-266-748A-156478	Sequence 156478,
	10	17.8	84.8	463	21	US-11-443-428A-160893	Sequence 160893,
	11	17.8	84.8	1120	14	US-11-266-748A-73083	Sequence 73083, A
c	12	17.8	84.8	1120	14	US-11-266-748A-125894	Sequence 125894,
	13	17.8	84.8	7896	11	US-10-528-311-4	Sequence 4, Appli
c	14	17.8	84.8	86592	11	US-10-497-268-1	Sequence 1, Appli
	15	17.4	82.9	2000	10	US-10-750-622-33522	Sequence 33522, A
	16	16.8	80.0	201	6	US-10-990-328-118786	Sequence 118786,
c	17	16.8	80.0	240	21	US-11-497-489A-51738	Sequence 51738, A
	18	16.8	80.0	398	21	US-11-497-489A-28993	Sequence 28993, A
c	19	16.8	80.0	488	14	US-11-266-748A-178608	Sequence 178608,
	20	16.8	80.0	488	14	US-11-266-748A-246340	Sequence 246340,
c	21	16.8	80.0	488	14	US-11-266-748A-263857	Sequence 263857,
	22	16.8	80.0	488	14	US-11-266-748A-324374	Sequence 324374,
	23	16.8	80.0	494	21	US-11-443-428A-409401	Sequence 409401,
c	24	16.8	80.0	619	14	US-11-266-748A-5478	Sequence 5478, Ap
c	25	16.8	80.0	657	21	US-11-443-428A-123464	Sequence 123464,
c	26	16.8	80.0	676	14	US-11-266-748A-359762	Sequence 359762,
	27	16.8	80.0	676	14	US-11-266-748A-443141	Sequence 443141,
	28	16.8	80.0	898	21	US-11-443-428A-72587	Sequence 72587, A
c	29	16.8	80.0	1076	14	US-11-266-748A-79710	Sequence 79710, A
	30	16.8	80.0	1076	14	US-11-266-748A-132521	Sequence 132521,
	31	16.8	80.0	1500	13	US-11-635-706-11241	Sequence 11241, A
c	32	16.8	80.0	1932	15	US-11-056-355B-89925	Sequence 89925, A
c	33	16.8	80.0	1932	15	US-11-056-355B-93681	Sequence 93681, A
	34	16.8	80.0	2671	15	US-11-218-305-10585	Sequence 10585, A
c	35	16.8	80.0	3956	14	US-11-266-748A-24661	Sequence 24661, A
c	36	16.8	80.0	3971	21	US-11-443-428A-123462	Sequence 123462,
c	37	16.8	80.0	4025	21	US-11-443-428A-123461	Sequence 123461,
c	38	16.8	80.0	4389	21	US-11-443-428A-123463	Sequence 123463,
	39	16.8	80.0	4789	14	US-11-266-748A-27829	Sequence 27829, A
c	40	16.8	80.0	12858	6	US-10-990-328-96819	Sequence 96819, A
	41	16.8	80.0	35218	6	US-10-990-328-93486	Sequence 93486, A
	42	16.8	80.0	49186	10	US-10-796-280-12576	Sequence 12576, A
	43	16.8	80.0	56319	10	US-10-767-471-10618	Sequence 10618, A
	44	16.8	80.0	56324	20	US-11-066-316A-9912	Sequence 9912, Ap
	45	16.8	80.0	129336	6	US-10-990-328-97125	Sequence 97125, A

ALIGNMENTS

RESULT 1
US-10-529-447-5

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 844 Seconds
                                          (without alignments)
                                          297.960 Million cell updates/sec

Title: US-10-529-447-4
Perfect score: 24
Sequence: 1 tacacttgggttttcagtacgaggt 24

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length:. 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	8	US-10-529-447-4	Sequence 4, Appli
c	2	18.2	75.8	2356	10	US-10-750-622-61747	Sequence 61747, A
	3	17.6	73.3	455	21	US-11-497-489A-79378	Sequence 79378, A
	4	17.6	73.3	4663	11	US-10-540-898-405	Sequence 405, App
c	5	17.6	73.3	6574	21	US-11-443-428A-23440	Sequence 23440, A
c	6	17.6	73.3	7808	11	US-10-959-175-4	Sequence 4, Appli
	7	17.2	71.7	201	6	US-10-990-328-195898	Sequence 195898,
c	8	17.2	71.7	201	11	US-10-284-444-5751	Sequence 5751, Ap
c	9	17.2	71.7	702	21	US-11-443-428A-692003	Sequence 692003,
c	10	17.2	71.7	1299	21	US-11-443-428A-97151	Sequence 97151, A
	11	17.2	71.7	22244	6	US-10-990-328-98021	Sequence 98021, A
	12	17.2	71.7	69867	6	US-10-990-328-94190	Sequence 94190, A
c	13	17.2	71.7	131760	6	US-10-990-328-94636	Sequence 94636, A
	14	16.8	70.0	301	14	US-11-266-748A-93656	Sequence 93656, A
c	15	16.8	70.0	301	14	US-11-266-748A-146467	Sequence 146467,
c	16	16.8	70.0	301	21	US-11-443-428A-259505	Sequence 259505,
	17	16.8	70.0	669	20	US-11-503-243A-267569	Sequence 267569,
	18	16.8	70.0	709	20	US-11-433-832-29435	Sequence 29435, A
c	19	16.8	70.0	936	20	US-11-503-243A-132509	Sequence 132509,
	20	16.8	70.0	1541	11	US-10-953-349-11334	Sequence 11334, A
	21	16.8	70.0	1541	15	US-11-056-355B-48963	Sequence 48963, A
	22	16.8	70.0	1606	15	US-11-056-355B-46930	Sequence 46930, A
	23	16.8	70.0	1606	15	US-11-056-355B-50119	Sequence 50119, A
	24	16.8	70.0	36929	6	US-10-990-328-95503	Sequence 95503, A
	25	16.8	70.0	36929	20	US-11-066-316A-10008	Sequence 10008, A
c	26	16.8	70.0	194266	11	US-10-833-833-15	Sequence 15, Appl
c	27	16.6	69.2	443	16	US-11-354-263-11	Sequence 11, Appl
	28	16.6	69.2	473	21	US-11-443-428A-226145	Sequence 226145,
	29	16.6	69.2	585	21	US-11-443-428A-170156	Sequence 170156,
	30	16.6	69.2	601	7	US-10-940-774-81581	Sequence 81581, A
	31	16.6	69.2	601	7	US-10-940-774-87580	Sequence 87580, A
c	32	16.6	69.2	601	7	US-10-940-774-156414	Sequence 156414,
c	33	16.6	69.2	701	10	US-10-750-622-28206	Sequence 28206, A
c	34	16.6	69.2	918	14	US-11-266-748A-247385	Sequence 247385,
	35	16.6	69.2	919	21	US-11-443-428A-478175	Sequence 478175,
	36	16.6	69.2	1000	14	US-11-266-748A-203882	Sequence 203882,
	37	16.6	69.2	1501	5	US-09-815-264-31720	Sequence 31720, A
	38	16.6	69.2	1501	13	US-11-595-983-31720	Sequence 31720, A
c	39	16.6	69.2	1549	16	US-11-354-263-12	Sequence 12, Appl
	40	16.6	69.2	1647	13	US-11-516-230-289	Sequence 289, App
	41	16.6	69.2	1647	13	US-11-516-230-12214	Sequence 12214, A
	42	16.6	69.2	2068	12	US-10-703-032-26771	Sequence 26771, A
c	43	16.6	69.2	2233	6	US-10-777-288A-1116	Sequence 1116, Ap
	44	16.6	69.2	2593	15	US-11-218-305-17498	Sequence 17498, A
	45	16.6	69.2	2790	10	US-10-750-622-64091	Sequence 64091, A

ALIGNMENTS

RESULT 1
US-10-529-447-4

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:53:33 ; Search time 773 Seconds
                                       (without alignments)
                                 297.960 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16466727 seqs, 5237448290 residues

Total number of hits satisfying chosen parameters: 32933454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	100.0	22	8	US-10-529-447-3	Sequence 3, Appli
c	2	18.8	85.5	54	6	US-10-951-241-133	Sequence 133, App
	3	18.8	85.5	2694	15	US-11-218-305-3959	Sequence 3959, Ap
	4	17.8	80.9	357	21	US-11-497-489A-23771	Sequence 23771, A
	5	17.8	80.9	1112	21	US-11-443-428A-596881	Sequence 596881,
	6	17.8	80.9	1197	21	US-11-443-428A-412618	Sequence 412618,
	7	17.8	80.9	2380	21	US-11-443-428A-596879	Sequence 596879,
	8	17.8	80.9	2561	21	US-11-443-428A-596883	Sequence 596883,
c	9	17.2	78.2	102	15	US-11-333-738-75	Sequence 75, Appl
c	10	17.2	78.2	294	21	US-11-497-489A-7324	Sequence 7324, Ap
c	11	17.2	78.2	368	21	US-11-497-489A-50703	Sequence 50703, A
c	12	17.2	78.2	395	21	US-11-497-489A-154456	Sequence 154456,
c	13	17.2	78.2	458	21	US-11-497-489A-119792	Sequence 119792,
	14	17.2	78.2	460	21	US-11-497-489A-83727	Sequence 83727, A
c	15	17.2	78.2	1670	18	US-11-241-607-61902	Sequence 61902, A
c	16	17.2	78.2	1670	18	US-11-241-607-61902	Sequence 61902, A
c	17	17.2	78.2	38831	5	US-09-815-264-78651	Sequence 78651, A
c	18	17.2	78.2	38831	13	US-11-595-983-78651	Sequence 78651, A
c	19	17.2	78.2	38831	18	US-11-491-125A-7942	Sequence 7942, Ap
c	20	17.2	78.2	1078171	9	US-10-915-727-12215	Sequence 12215, A
c	21	17	77.3	924430	9	US-10-915-727-12216	Sequence 12216, A
c	22	16.8	76.4	132	20	US-11-503-243A-107946	Sequence 107946,
	23	16.8	76.4	354	21	US-11-497-489A-4023	Sequence 4023, Ap
c	24	16.8	76.4	658	14	US-11-266-748A-72599	Sequence 72599, A
	25	16.8	76.4	658	14	US-11-266-748A-125410	Sequence 125410,
c	26	16.4	74.5	32	6	US-10-535-164-242960	Sequence 242960,
c	27	16.4	74.5	201	6	US-10-990-328-298078	Sequence 298078,
	28	16.4	74.5	202	21	US-11-443-428A-627698	Sequence 627698,
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c	33	16.4	74.5	1097	21	US-11-443-428A-53361	Sequence 53361, A
c	34	16.4	74.5	1363	21	US-11-443-428A-53350	Sequence 53350, A
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c	43	16.4	74.5	2091	21	US-11-443-428A-53344	Sequence 53344, A
c	44	16.4	74.5	2094	21	US-11-443-428A-53343	Sequence 53343, A
c	45	16.4	74.5	2328	21	US-11-443-428A-28515	Sequence 28515, A

ALIGNMENTS

RESULT 1
US-10-529-447-3

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 739 Seconds
                                          (without alignments)
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Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
         1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

                       %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   22.4   86.2   25 15   US-11-121-849-397932   Sequence 397932,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 739 Seconds
                                         (without alignments)
                                         432.471 Million cell updates/sec

Title: US-10-529-447-23
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
              1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
              2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
              3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
              4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
              5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
              6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
              7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
              8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
              9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
             10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
             11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
             12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
             13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
             14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
             15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
             16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                          %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   22.4   86.2   25   15   US-11-121-849-397932   Sequence 397932,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 653 Seconds
                                          (without alignments)
                                          432.471 Million cell updates/sec

Title: US-10-529-447-22
Perfect score: 23
Sequence: 1 ctccaacatgctatgcaacgtcc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
          1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
          9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
         10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
         11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
         12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
         13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
         14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
         15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                          %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   23   100.0   33 9   US-10-311-645A-79   Sequence 79, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 625 Seconds
                                        (without alignments)
                                        432.471 Million cell updates/sec

Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
          1:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          3:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          8:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
          9:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
         10:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
         11:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
         12:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
         13:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
         14:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
         15:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         16:    /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
c   1   22   100.0   25   15   US-11-121-849-397935   Sequence 397935,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 597 Seconds
                                          (without alignments)
                                          432.471 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
        1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
        2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
        3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
        4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
        5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
        6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
        7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
        8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
        9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
       10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
       11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
       12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
       13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
       14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
       15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
       16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   17.8   84.8   597 4   US-09-925-065A-371335   Sequence 371335,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 597 Seconds
                                          (without alignments)
                                          432.471 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
         1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                             SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   18   85.7   25 15   US-11-121-849-397931   Sequence 397931,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 597 Seconds
                                        (without alignments)
                                        432.471 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
               1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
               2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
               3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
               4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
               5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
               6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
               7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
               8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
               9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
               10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
               11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
               12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
               13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
               14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
               15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
               16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   18   85.7   25   15   US-11-121-849-397931   Sequence 397931,

```
                        GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on:            July 16, 2007, 09:47:19 ; Search time 682 Seconds
                                            (without alignments)
                                            432.471 Million cell updates/sec

Title:             US-10-529-447-4
Perfect score:     24
Sequence:          1 tacacttgggtttcagtacgaggt 24

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         Published_Applications_NA_Main:*
         1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
         2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
         3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
         4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
         5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
         6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
         7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
         8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
         9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
        10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
        11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
        12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
        13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
        14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
        15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
        16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	24	100.0	474	11	US-10-530-253-43	Sequence 43, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:47:19 ; Search time 625 Seconds
                                          (without alignments)
                                          432.471 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
          1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
          2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
          3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
          4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
          5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
          6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
          7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
          8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
          9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
         10:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
         11:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
         12:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
         13:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
         14:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
         15:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
         16:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
     1   22   100.0   474 11   US-10-530-253-43   Sequence 43, Appl

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 203 Seconds
                                          (without alignments)
                                          462.052 Million cell updates/sec

Title: US-10-529-447-24
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	19.8	76.2	517	6	US-09-925-065A-524953	Sequence 524953,
c	2	19.6	75.4	631	6	US-09-925-065A-524804	Sequence 524804,
	3	19.2	73.8	430	5	US-10-703-032-85228	Sequence 85228, A
c	4	18.8	72.3	523	6	US-09-925-065A-116688	Sequence 116688,
	5	18.8	72.3	578	6	US-09-925-065A-320131	Sequence 320131,
c	6	18.6	71.5	564	6	US-09-925-065A-790390	Sequence 790390,
c	7	18.6	71.5	565	6	US-09-925-065A-790380	Sequence 790380,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 203 Seconds
                                          (without alignments)
                                          462.052 Million cell updates/sec

Title: US-10-529-447-23
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                  1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                  2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                  3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                  4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                  5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                  6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                  7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                  8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                  9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                  10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB ID   Description
    ----
      1   19.8   76.2   517   6   US-09-925-065A-524953   Sequence 524953,
  c   2   19.6   75.4   631   6   US-09-925-065A-524804   Sequence 524804,
      3   19.2   73.8   430   5   US-10-703-032-85228   Sequence 85228, A
  c   4   18.8   72.3   523   6   US-09-925-065A-116688   Sequence 116688,
      5   18.8   72.3   578   6   US-09-925-065A-320131   Sequence 320131,
  c   6   18.6   71.5   564   6   US-09-925-065A-790390   Sequence 790390,
  c   7   18.6   71.5   565   6   US-09-925-065A-790380   Sequence 790380,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 180 Seconds
                                         (without alignments)
                                         462.052 Million cell updates/sec

Title: US-10-529-447-22
Perfect score: 23
Sequence: 1 ctccaacatgctatgcaacgtcc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1:   /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9:   /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
     No.   Score Match Length DB ID   Description
        ----
     c 1   23 100.0   474 5 US-10-530-253-43   Sequence 43, Appl
        2   17.8   77.4   2065 3 US-09-618-425-12   Sequence 12, Appl
     c 3   17.4   75.7 312957 3 US-09-949-001-31   Sequence 31, Appl
     c 4   17.4   75.7 312972 3 US-09-949-001-34   Sequence 34, Appl
     c 5   16.8   73.0   579 6 US-09-925-065A-606210   Sequence 606210,
     c 6   16.8   73.0   579 6 US-09-925-065A-606211   Sequence 606211,
     c 7   16.8   73.0   579 6 US-09-925-065A-606212   Sequence 606212,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 172 Seconds
                                        (without alignments)
                                        462.052 Million cell updates/sec

Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
               1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
               2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
               3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
               4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
               5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
               6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
               7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
               8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
               9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
               10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17.8	80.9	358	6	US-09-925-065A-318135	Sequence 318135,
c 2	17.8	80.9	566	6	US-09-925-065A-620212	Sequence 620212,
3	17.8	80.9	6924	2	US-08-015-973-2	Sequence 2, Appli
4	17.8	80.9	6924	2	US-08-448-164-2	Sequence 2, Appli
5	17.8	80.9	7941	3	US-09-816-703A-1	Sequence 1, Appli
6	17.8	80.9	7941	5	US-10-652-981-5	Sequence 5, Appli
7	17.8	80.9	8058	5	US-10-652-981-3	Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 164 Seconds
                                           (without alignments)
                                           462.052 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1:   /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9:   /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description
   ----
       1   17.8   84.8   597   6   US-09-925-065A-371335   Sequence 371335,
       2   16.8   80.0   452   5   US-10-703-032-42891   Sequence 42891, A
  c   3   16.8   80.0   564   6   US-09-925-065A-867689   Sequence 867689,
  c   4   16.8   80.0   568   6   US-09-925-065A-865926   Sequence 865926,
       5   16.8   80.0   573   6   US-09-925-065A-866206   Sequence 866206,
  c   6   16.8   80.0   574   6   US-09-925-065A-473767   Sequence 473767,
  c   7   16.8   80.0   574   6   US-09-925-065A-473768   Sequence 473768,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 164 Seconds
                                           (without alignments)
                                           462.052 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16.8	80.0	493	6	US-09-925-065A-737714	Sequence 737714,
2	16.8	80.0	493	6	US-09-925-065A-814818	Sequence 814818,
3	16.8	80.0	520	6	US-09-925-065A-10905	Sequence 10905, A
4	16.8	80.0	522	6	US-09-925-065A-767195	Sequence 767195,
5	16.8	80.0	522	6	US-09-925-065A-767196	Sequence 767196,
6	16.8	80.0	546	6	US-09-925-065A-13239	Sequence 13239, A
c 7	16.8	80.0	590	6	US-09-925-065A-294764	Sequence 294764,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 164 Seconds
                                        (without alignments)
                                        462.052 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
      1   16.8   80.0   493   6   US-09-925-065A-737714   Sequence 737714,
      2   16.8   80.0   493   6   US-09-925-065A-814818   Sequence 814818,
      3   16.8   80.0   520   6   US-09-925-065A-10905   Sequence 10905, A
      4   16.8   80.0   522   6   US-09-925-065A-767195   Sequence 767195,
      5   16.8   80.0   522   6   US-09-925-065A-767196   Sequence 767196,
      6   16.8   80.0   546   6   US-09-925-065A-13239   Sequence 13239, A
c   7   16.8   80.0   590   6   US-09-925-065A-294764   Sequence 294764,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 188 Seconds
                                          (without alignments)
                                          462.052 Million cell updates/sec

Title: US-10-529-447-4
Perfect score: 24
Sequence: 1 tacacttgggtttcagtacgaggt 24

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

7,223,408

                                         SUMMARIES
                          %
Result   Query
   No.   Score Match Length DB ID   Description
      ----
   c 1   24 100.0   474 5   US-10-530-253-43   Sequence 43, Appl
   c 2   18.2   75.8   528 6   US-09-925-065A-122108   Sequence 122108,
   c 3   18.2   75.8   528 6   US-09-925-065A-122109   Sequence 122109,
   c 4   17.6   73.3   456 5   US-10-530-253-48   Sequence 48, Appl
      5   17.6   73.3   571 6   US-09-925-065A-329804   Sequence 329804,
   c 6   17.2   71.7   531 6   US-09-925-065A-760285   Sequence 760285,
   c 7   17.2   71.7   543 6   US-09-925-065A-802057   Sequence 802057,

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:43:10 ; Search time 172 Seconds
                                          (without alignments)
                                          462.052 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2773932 seqs, 1806713642 residues

Total number of hits satisfying chosen parameters: 5547864

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1:   /EMC_Celerra_SIDS3/ptodata/1/ina/1_COMB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/1/ina/5_COMB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/1/ina/6A_COMB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/1/ina/6B_COMB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/1/ina/7_COMB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/1/ina/H_COMB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/1/ina/PCTUS_COMB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/1/ina/PP_COMB.seq:*
                 9:   /EMC_Celerra_SIDS3/ptodata/1/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	474	5	US-10-530-253-43	Sequence 43, Appl
2	17.4	79.1	500	6	US-09-925-065A-761311	Sequence 761311,
3	17.2	78.2	90	3	US-09-419-381-89	Sequence 89, Appl
4	17.2	78.2	450	5	US-10-530-253-45	Sequence 45, Appl
c 5	17.2	78.2	575	6	US-09-925-065A-850687	Sequence 850687,
6	16.4	74.5	250	3	US-09-439-313-409	Sequence 409, App
7	16.4	74.5	250	3	US-09-352-616A-409	Sequence 409, App

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2960 Seconds
                                          (without alignments)
                                 545.032 Million cell updates/sec

Title: US-10-529-447-24
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	26	100.0	376	3	BI255229	BI255229 602978346
	2	26	100.0	771	3	BI224324	BI224324 602940647
	3	26	100.0	833	5	BX400902	BX400902 BX400902
c	4	24.4	93.8	576	4	BQ380375	BQ380375 MR3-UT009
	5	24.4	93.8	584	4	BQ380269	BQ380269 MR3-UT009
	6	21.2	81.5	916	17	CL463721	CL463721 SAIL_11_B
	7	20.8	80.0	269	16	BZ753718	BZ753718 PUDCH70TB
	8	20.8	80.0	641	16	BZ751951	BZ751951 PUDCH94TB
	9	20.2	77.7	486	15	BH121949	BH121949 RPCI-24-3
c	10	20.2	77.7	753	18	DX455730	DX455730 MAMAX03TF
c	11	19.6	75.4	230	7	AW759523	AW759523 sl44e01.y
c	12	19.6	75.4	243	7	AW733847	AW733847 sk78b11.y
c	13	19.6	75.4	278	18	DX258610	DX258610 OR_ABa014
c	14	19.6	75.4	292	7	AW100332	AW100332 sd23b05.y
c	15	19.6	75.4	308	1	AA174824	AA174824 mt13f09.r
c	16	19.6	75.4	314	2	BG237114	BG237114 saa97e12.
	17	19.6	75.4	322	4	BU546867	BU546867 GM880007A
c	18	19.6	75.4	340	3	BI315908	BI315908 saf64h08.
c	19	19.6	75.4	374	19	DR10A1T	AL735076 Danio rer
	20	19.6	75.4	375	1	AI899873	AI899873 sb94e05.y
c	21	19.6	75.4	416	1	AI122505	AI122505 uc62c06.r
	22	19.6	75.4	437	11	.T58283	T58283 yb50b06.r1
c	23	19.6	75.4	439	7	AW781731	AW781731 sl90c11.y
	24	19.6	75.4	450	4	BQ640782	BQ640782 TVEST004.
c	25	19.6	75.4	457	1	AI604297	AI604297 mt13f09.y
c	26	19.6	75.4	471	13	DT084305	DT084305 89-PTE-37
	27	19.6	75.4	476	8	CD410801	CD410801 Gm_ck3912
c	28	19.6	75.4	492	5	BX517973	BX517973 BX517973
c	29	19.6	75.4	494	2	BE330011	BE330011 so72c11.y
	30	19.6	75.4	500	8	CD590328	CD590328 RK057A1F0
c	31	19.6	75.4	508	2	BG652028	BG652028 sad73b12.
	32	19.6	75.4	511	8	CF920702	CF920702 gmrhRww3-
c	33	19.6	75.4	514	3	BM731658	BM731658 sal82e02.
c	34	19.6	75.4	519	2	BG653120	BG653120 sad82b05.
c	35	19.6	75.4	533	8	CD416201	CD416201 Gm_ck6503
	36	19.6	75.4	562	8	CD412066	CD412066 Gm_ck4310
c	37	19.6	75.4	564	8	CF921926	CF921926 gmrhRww24
c	38	19.6	75.4	584	8	CF922574	CF922574 gmrhRww24
c	39	19.6	75.4	590	5	CA935166	CA935166 sau49e12.
	40	19.6	75.4	650	8	CD596207	CD596207 RK099A2F0
	41	19.6	75.4	653	19	DE189314	DE189314 Branchios
	42	19.6	75.4	655	8	CD428597	CD428597 ETH1_27_C
	43	19.6	75.4	686	19	DE205319	DE205319 Branchios
	44	19.6	75.4	715	19	AG450707	AG450707 Mus muscu
	45	19.6	75.4	758	9	CK238526	CK238526 AGENCOURT

ALIGNMENTS

RESULT 1
BI255229
LOCUS   BI255229   376 bp   mRNA   linear   EST 17-JUL-2001
DEFINITION   602978346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123458 5',
               mRNA sequence.

```
                         GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on:          July 16, 2007, 09:42:41 ; Search time 2960 Seconds
                                          (without alignments)
                                          545.032 Million cell updates/sec

Title:           US-10-529-447-23
Perfect score:   26
Sequence:        1 agagacagcacaggcattgttccatg 26

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters:      107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:  gb_est1:*
                 2:  gb_est3:*
                 3:  gb_est4:*
                 4:  gb_est5:*
                 5:  gb_est6:*
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                 7:  gb_est2:*
                 8:  gb_est7:*
                 9:  gb_est8:*
                 10:  gb_est9:*
                 11:  gb_est13:*
                 12:  gb_est12:*
                 13:  gb_est11:*
                 14:  gb_est10:*
                 15:  gb_gss1:*
                 16:  gb_gss2:*
                 17:  gb_gss3:*
                 18:  gb_gss4:*
                 19:  gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result          Query
```

	No.	Score	Match	Length	DB	ID	Description
	1	26	100.0	376	3	BI255229	BI255229 602978346
	2	26	100.0	771	3	BI224324	BI224324 602940647
	3	26	100.0	833	5	BX400902	BX400902 BX400902
c	4	24.4	93.8	576	4	BQ380375	BQ380375 MR3-UT009
	5	24.4	93.8	584	4	BQ380269	BQ380269 MR3-UT009
	6	21.2	81.5	916	17	CL463721	CL463721 SAIL_11_B
	7	20.8	80.0	269	16	BZ753718	BZ753718 PUDCH70TB
	8	20.8	80.0	641	16	BZ751951	BZ751951 PUDCH94TB
	9	20.2	77.7	486	15	BH121949	BH121949 RPCI-24-3
c	10	20.2	77.7	753	18	DX455730	DX455730 MAMAX03TF
c	11	19.6	75.4	230	7	AW759523	AW759523 sl44e01.y
c	12	19.6	75.4	243	7	AW733847	AW733847 sk78b11.y
c	13	19.6	75.4	278	18	DX258610	DX258610 OR_ABa014
c	14	19.6	75.4	292	7	AW100332	AW100332 sd23b05.y
c	15	19.6	75.4	308	1	AA174824	AA174824 mt13f09.r
c	16	19.6	75.4	314	2	BG237114	BG237114 saa97e12.
	17	19.6	75.4	322	4	BU546867	BU546867 GM880007A
c	18	19.6	75.4	340	3	BI315908	BI315908 saf64h08.
c	19	19.6	75.4	374	19	DR10A1T	AL735076 Danio rer
	20	19.6	75.4	375	1	AI899873	AI899873 sb94e05.y
c	21	19.6	75.4	416	1	AI122505	AI122505 uc62c06.r
	22	19.6	75.4	437	11	T58283	T58283 yb50b06.r1
c	23	19.6	75.4	439	7	AW781731	AW781731 sl90c11.y
	24	19.6	75.4	450	4	BQ640782	BQ640782 TVEST004.
c	25	19.6	75.4	457	1	AI604297	AI604297 mt13f09.y
c	26	19.6	75.4	471	13	DT084305	DT084305 89-PTE-37
	27	19.6	75.4	476	8	CD410801	CD410801 Gm_ck3912
c	28	19.6	75.4	492	5	BX517973	BX517973 BX517973
c	29	19.6	75.4	494	2	BE330011	BE330011 so72c11.y
	30	19.6	75.4	500	8	CD590328	CD590328 RK057A1F0
c	31	19.6	75.4	508	2	BG652028	BG652028 sad73b12.
	32	19.6	75.4	511	8	CF920702	CF920702 gmrhRww3-
c	33	19.6	75.4	514	3	BM731658	BM731658 sal82e02.
c	34	19.6	75.4	519	2	BG653120	BG653120 sad82b05.
c	35	19.6	75.4	533	8	CD416201	CD416201 Gm_ck6503
	36	19.6	75.4	562	8	CD412066	CD412066 Gm_ck4310
c	37	19.6	75.4	564	8	CF921926	CF921926 gmrhRww24
c	38	19.6	75.4	584	8	CF922574	CF922574 gmrhRww24
c	39	19.6	75.4	590	5	CA935166	CA935166 sau49e12.
	40	19.6	75.4	650	8	CD596207	CD596207 RK099A2F0
	41	19.6	75.4	653	19	DE189314	DE189314 Branchios
	42	19.6	75.4	655	8	CD428597	CD428597 ETH1_27_C
	43	19.6	75.4	686	19	DE205319	DE205319 Branchios
	44	19.6	75.4	715	19	AG450707	AG450707 Mus muscu
	45	19.6	75.4	758	9	CK238526	CK238526 AGENCOURT

ALIGNMENTS

RESULT 1
BI255229
LOCUS   BI255229   376 bp   mRNA   linear   EST 17-JUL-2001
DEFINITION   602978346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123458 5',
              mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2618 Seconds
                                          (without alignments)
                                          545.032 Million cell updates/sec

Title: US-10-529-447-22
Perfect score: 23
Sequence: 1 ctccaacatgctatgcaacgtcc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                            SUMMARIES
                       %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	20.4	88.7	198	18	DX732360	DX732360 2254838 V
c	2	20.4	88.7	349	18	DX636582	DX636582 2008220 V
	3	20.4	88.7	495	18	DX725768	DX725768 2470380 V
c	4	20.4	88.7	543	18	DX734121	DX734121 2349513 V
c	5	20.4	88.7	680	18	DX634126	DX634126 1949451 V
	6	20.4	88.7	681	18	DX703136	DX703136 2451996 V
	7	20.4	88.7	688	18	DX737448	DX737448 2478965 V
c	8	20.4	88.7	695	12	EB032368	EB032368 lk_hhlvxx
c	9	19.4	84.3	841	18	DX356712	DX356712 ZMMBBc001
c	10	18.8	81.7	350	18	DX623316	DX623316 2299440 V
c	11	18.8	81.7	465	13	DR786971	DR786971 ZM_BFb000
	12	18.8	81.7	566	10	CV094207	CV094207 FAMU_USDA
	13	18.8	81.7	738	10	CV098346	CV098346 FAMU_USDA
c	14	18.8	81.7	882	18	CW974799	CW974799 AIAA-aaa7
c	15	18.4	80.0	405	17	CG395158	CG395158 ZMMBBc001
c	16	18.4	80.0	490	8	CB277674	CB277674 ks38g05.y
c	17	18.4	80.0	571	8	CB277673	CB277673 ks38g04.y
c	18	18.4	80.0	939	17	CG167013	CG167013 PUKDW82TB
c	19	18.2	79.1	415	15	AQ690103	AQ690103 nbxb0081I
	20	18.2	79.1	520	2	BE680466	BE680466 df80f01.y
c	21	18.2	79.1	680	17	CL797631	CL797631 OR_CBa000
c	22	18.2	79.1	682	18	DU413516	DU413516 109841572
	23	18.2	79.1	688	17	CW133515	CW133515 104_517_1
c	24	18.2	79.1	692	18	CZ002295	CZ002295 OA_BBa005
c	25	18.2	79.1	697	18	CZ147995	CZ147995 OA_BBa005
c	26	18.2	79.1	716	15	AQ574067	AQ574067 nbxb0085G
	27	18.2	79.1	717	5	CA086464	CA086464 SCMCAM208
c	28	18.2	79.1	717	14	DB493205	DB493205 DB493205
c	29	18.2	79.1	730	17	CL808489	CL808489 OR_CBa002
c	30	18.2	79.1	738	17	CL855192	CL855192 OR_CBa008
	31	18.2	79.1	747	17	CE345416	CE345416 tigr-gss-
	32	18.2	79.1	750	12	EB466319	EB466319 AGENCOURT
c	33	18.2	79.1	769	17	CW505893	CW505893 OP__Ba000
	34	18.2	79.1	779	5	BX846024	BX846024 BX846024
c	35	18.2	79.1	786	15	AQ574047	AQ574047 nbxb0085E
c	36	18.2	79.1	814	17	CL809783	CL809783 OR_CBa002
	37	18.2	79.1	846	12	EB647374	EB647374 AGENCOURT
	38	18.2	79.1	877	18	CZ226783	CZ226783 AIAA-aaf1
	39	18.2	79.1	937	18	CZ323786	CZ323786 ZMMBF0027
c	40	18.2	79.1	1146	9	CK206137	CK206137 FGAS01771
	41	18	78.3	636	17	CL823430	CL823430 OR_CBa004
	42	18	78.3	776	17	CW667404	CW667404 OG_BBa002
c	43	17.8	77.4	522	16	BZ681678	BZ681678 PUBDQ29TD
	44	17.8	77.4	528	1	AI488797	AI488797 EST247136
	45	17.8	77.4	553	2	BF021503	BF021503 uy35h11.y

ALIGNMENTS

RESULT 1
DX732360
LOCUS   DX732360   198 bp   DNA   linear   GSS 30-MAY-2006
DEFINITION   2254838 VV03 Ustilago maydis genomic clone 909989, genomic survey
               sequence.

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2504 Seconds
                                        (without alignments)
                                  545.032 Million cell updates/sec

Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
c	1	18.8	85.5	351	3	BJ833988	BJ833988 BJ833988
	2	18.8	85.5	392	3	BJ822812	BJ822812 BJ822812
c	3	18.8	85.5	414	15	AZ146457	AZ146457 SP_0021_B
c	4	18.4	83.6	327	3	BI189155	BI189155 e2a01fs.r
	5	18.4	83.6	431	2	BF008791	BF008791 ss69d12.y
c	6	18.4	83.6	481	17	CL881868	CL881868 abf51h08.
	7	18.4	83.6	488	2	BG046824	BG046824 saa62c02.
	8	18.4	83.6	511	4	BQ630546	BQ630546 saq08g09.
	9	18.4	83.6	553	17	CE826896	CE826896 tigr-gss-
	10	18.4	83.6	572	4	BQ630329	BQ630329 saq05h10.
	11	18.4	83.6	580	8	CF807719	CF807719 psHB027xK
c	12	18.4	83.6	773	12	EB556583	EB556583 AGENCOURT
c	13	18.4	83.6	838	19	AG880133	AG880133 Oryza sat
c	14	18	81.8	380	15	AZ906387	AZ906387 RPCI-24-1
	15	18	81.8	622	19	BX969561	BX969561 Forward s
	16	18	81.8	675	2	BG695633	BG695633 NISC_iv19
	17	18	81.8	784	19	CR242670	CR242670 Forward s
	18	18	81.8	806	19	BX983339	BX983339 Forward s
	19	17.8	80.9	366	17	CE356706	CE356706 tigr-gss-
c	20	17.8	80.9	369	13	DR383395	DR383395 13802170
c	21	17.8	80.9	376	3	BI255229	BI255229 602978346
	22	17.8	80.9	388	7	AU227466	AU227466 AU227466
c	23	17.8	80.9	409	16	CC054721	CC054721 SALK_0799
	24	17.8	80.9	420	15	AQ573168	AQ573168 HS_2125_A
	25	17.8	80.9	445	4	BP586393	BP586393 BP586393
c	26	17.8	80.9	452	2	BF561865	BF561865 UI-R-C2-n
	27	17.8	80.9	509	6	AB224819	AB224819 Aspergill
	28	17.8	80.9	525	7	AV547647	AV547647 AV547647
c	29	17.8	80.9	526	1	AA394460	AA394460 26127 Lam
	30	17.8	80.9	536	14	DA103421	DA103421 DA103421
	31	17.8	80.9	537	18	CW973376	CW973376 AIAA-aaa6
	32	17.8	80.9	542	7	AW643566	AW643566 cm31c03.w
	33	17.8	80.9	543	14	DA803912	DA803912 DA803912
	34	17.8	80.9	544	7	AW643555	AW643555 cm31b03.w
	35	17.8	80.9	544	14	DA413665	DA413665 DA413665
	36	17.8	80.9	546	14	DB089349	DB089349 DB089349
	37	17.8	80.9	553	14	DA802261	DA802261 DA802261
	38	17.8	80.9	554	14	DA188957	DA188957 DA188957
c	39	17.8	80.9	557	8	CB650395	CB650395 OSJNEb14N
	40	17.8	80.9	558	14	DA496246	DA496246 DA496246
	41	17.8	80.9	558	15	AZ092676	AZ092676 RPCI-23-4
	42	17.8	80.9	559	14	DA495963	DA495963 DA495963
	43	17.8	80.9	560	1	AL707478	AL707478 DKFZp686B
	44	17.8	80.9	563	5	BX845256	BX845256 BX845256
	45	17.8	80.9	563	9	CN418529	CN418529 170005325

ALIGNMENTS

RESULT 1
BJ833988/c
LOCUS   BJ833988   351 bp   mRNA   linear   EST 13-MAY-2005
DEFINITION   BJ833988 Yasufumi Emori unpublished cDNA library, olfactory
               epithelium Misgurnus anguillicaudatus cDNA clone dj20m15 3', mRNA

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2390 Seconds
                                          (without alignments)
                                          545.032 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

No.		Score	Match	Length	DB	ID	Description
c	1	21	100.0	376	3	BI255229	BI255229 602978346
	2	21	100.0	576	4	BQ380375	BQ380375 MR3-UT009
c	3	21	100.0	674	3	BI334876	BI334876 602998722
c	4	21	100.0	731	3	BI333662	BI333662 602999122
c	5	21	100.0	771	3	BI224324	BI224324 602940647
	6	19.4	92.4	777	8	CF406855	CF406855 CH3#044_G
	7	17.8	84.8	243	10	CV324193	CV324193 CM4-CT051
c	8	17.8	84.8	370	9	CI527379	CI527379 CI527379
c	9	17.8	84.8	431	9	CI533348	CI533348 CI533348
	10	17.8	84.8	433	15	AZ224543	AZ224543 RPCI-23-7
c	11	17.8	84.8	466	15	AZ118258	AZ118258 RPCI-23-2
c	12	17.8	84.8	473	1	AL917841	AL917841 AL917841
	13	17.8	84.8	489	15	AZ877129	AZ877129 2M0192L24
c	14	17.8	84.8	540	15	AQ999546	AQ999546 RPCI-23-3
c	15	17.8	84.8	542	15	AZ278698	AZ278698 RPCI-23-1
c	16	17.8	84.8	550	15	AQ920432	AQ920432 RPCI-23-2
c	17	17.8	84.8	554	15	AZ272556	AZ272556 RPCI-23-1
c	18	17.8	84.8	560	7	AW422622	AW422622 fi44f09.y
c	19	17.8	84.8	560	15	AQ983015	AQ983015 RPCI-23-2
	20	17.8	84.8	598	17	CE693305	CE693305 tigr-gss-
	21	17.8	84.8	612	15	AZ488818	AZ488818 1M0319K14
c	22	17.8	84.8	626	15	AZ062492	AZ062492 RPCI-23-4
	23	17.8	84.8	627	19	CR152690	CR152690 Reverse s
c	24	17.8	84.8	669	15	AZ555008	AZ555008 RPCI-23-2
c	25	17.8	84.8	670	15	AZ236842	AZ236842 RPCI-23-8
	26	17.8	84.8	697	15	BH121544	BH121544 RPCI-24-3
	27	17.8	84.8	706	15	AZ876886	AZ876886 2M0192B17
c	28	17.8	84.8	713	19	AG508171	AG508171 Mus muscu
	29	17.8	84.8	723	19	AG338753	AG338753 Mus muscu
c	30	17.8	84.8	725	19	AG367185	AG367185 Mus muscu
c	31	17.8	84.8	729	19	AG525917	AG525917 Mus muscu
c	32	17.8	84.8	739	19	AG428185	AG428185 Mus muscu
c	33	17.8	84.8	742	19	AG458915	AG458915 Mus muscu
	34	17.8	84.8	752	19	AG560725	AG560725 Mus muscu
	35	17.8	84.8	758	15	BH035221	BH035221 RPCI-24-2
c	36	17.8	84.8	764	19	AG469927	AG469927 Mus muscu
c	37	17.8	84.8	784	10	CT584999	CT584999 CT584999
c	38	17.8	84.8	852	18	DX243747	DX243747 OR_ABa012
c	39	17.4	82.9	319	4	BW120455	BW120455 BW120455
c	40	17.4	82.9	402	19	CNS01P2H	AL154281 Anopheles
c	41	17.4	82.9	421	17	CG569943	CG569943 OST198428
	42	17.4	82.9	437	3	BI220366	BI220366 602935663
	43	17.4	82.9	530	2	BE298458	BE298458 601119261
	44	17.4	82.9	533	2	BE448956	BE448956 ut50c10.y
	45	17.4	82.9	651	5	BW255875	BW255875 BW255875

ALIGNMENTS

RESULT 1
BI255229/c
LOCUS   BI255229   376 bp   mRNA   linear   EST 17-JUL-2001
DEFINITION   602978346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123458 5',
             mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2390 Seconds
                                          (without alignments)
                                          545.032 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID		Description
	1	21	100.0	376	3	BI255229	✓	BI255229 602978346
c	2	21	100.0	576	4	BQ380375	✓	BQ380375 MR3-UT009
	3	21	100.0	584	4	BQ380269		BQ380269 MR3-UT009
	4	21	100.0	674	3	BI334876	✓	BI334876 602998722
	5	21	100.0	731	3	BI333662	✓	BI333662 602999122
	6	21	100.0	771	3	BI224324	✓	BI224324 602940647
	7	21	100.0	833	5	BX400902		BX400902 BX400902
c	8	19.4	92.4	395	11	H65415		H65415 yu63c12.r1
	9	19	90.5	83	17	CG640484		CG640484 OST373269
c	10	19	90.5	601	18	DX493571		DX493571 Cpl35424
c	11	18.4	87.6	191	12	DY797376		DY797376 PMAL-aaa7
c	12	18.4	87.6	255	7	BB167452		BB167452 BB167452
	13	18.4	87.6	639	5	BW774400		BW774400 BW774400
c	14	18.4	87.6	670	9	CK933016		CK933016 CGF100434
c	15	18.4	87.6	743	15	AZ343434		AZ343434 1M0076P15
c	16	18.4	87.6	1177	16	CC290526		CC290526 CH261-172
	17	18.4	87.6	3176	6	AK030563		AK030563 Mus muscu
c	18	18	85.7	333	18	DU730974		DU730974 5F10_ENSD
c	19	18	85.7	646	15	AZ574416		AZ574416 328PvD11
c	20	18	85.7	746	11	EC607094		EC607094 Y70B12 YL
c	21	18	85.7	752	11	EC603953		EC603953 Y67D08 YL
	22	18	85.7	958	19	CNS02HZE		AL198275 Tetraodon
	23	18	85.7	1092	19	CNS05SXK		AL352433 Tetraodon
c	24	17.8	84.8	344	2	BF876167		BF876167 CM4-ET009
	25	17.8	84.8	453	2	BF876166		BF876166 CM4-ET009
	26	17.8	84.8	517	19	DE015081		DE015081 Branchios
c	27	17.8	84.8	541	2	BG864692		BG864692 602798388
	28	17.8	84.8	580	9	CK094803		CK094803 I055P43.3
c	29	17.8	84.8	597	3	BI124855		BI124855 I051P88P
c	30	17.8	84.8	620	9	CK104788		CK104788 I055P43.5
c	31	17.8	84.8	622	11	EE054461		EE054461 zf_30d3k_
c	32	17.8	84.8	625	3	BI125081		BI125081 I055P43P
c	33	17.8	84.8	748	15	AQ040360		AQ040360 CIT-HSP-2
c	34	17.8	84.8	800	9	CK477879		CK477879 AGENCOURT
c	35	17.8	84.8	821	18	CW996363		CW996363 OA_BBa007
c	36	17.8	84.8	849	9	CK310543		CK310543 SB02006B1
c	37	17.8	84.8	904	15	AQ787944		AQ787944 HS_3081_A
c	38	17.8	84.8	974	4	BQ944939		BQ944939 AGENCOURT
c	39	17.8	84.8	1299	12	DY301659		DY301659 KN0AAQ13Y
	40	17.8	84.8	1350	13	DN695090		DN695090 CGX98-A05
	41	17.4	82.9	253	3	BI382074		BI382074 BFLG2_000
	42	17.4	82.9	308	7	BB286061		BB286061 BB286061
	43	17.4	82.9	421	18	DX314559		DX314559 OR_ABa022
	44	17.4	82.9	438	5	BY382585		BY382585 BY382585
	45	17.4	82.9	494	16	CE014820		CE014820 tigr-gss-

ALIGNMENTS

RESULT 1
BI255229
LOCUS   BI255229   376 bp   mRNA   linear   EST 17-JUL-2001
DEFINITION 602978346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123458 5',
            mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2390 Seconds
                                   (without alignments)
                                 545.032 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                    %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	21	100.0	376	3	BI255229	BI255229 602978346
c	2	21	100.0	576	4	BQ380375	BQ380375 MR3-UT009
	3	21	100.0	584	4	BQ380269	BQ380269 MR3-UT009
	4	21	100.0	674	3	BI334876	BI334876 602998722
	5	21	100.0	731	3	BI333662	BI333662 602999122
	6	21	100.0	771	3	BI224324	BI224324 602940647
	7	21	100.0	833	5	BX400902	BX400902 BX400902
c	8	19.4	92.4	395	11	H65415	H65415 yu63c12.r1
	9	19	90.5	83	17	CG640484	CG640484 OST373269
c	10	19	90.5	601	18	DX493571	DX493571 Cpl35424
c	11	18.4	87.6	191	12	DY797376	DY797376 PMAL-aaa7
c	12	18.4	87.6	255	7	BB167452	BB167452 BB167452
	13	18.4	87.6	639	5	BW774400	BW774400 BW774400
c	14	18.4	87.6	670	9	CK933016	CK933016 CGF100434
c	15	18.4	87.6	743	15	AZ343434	AZ343434 1M0076P15
c	16	18.4	87.6	1177	16	CC290526	CC290526 CH261-172
	17	18.4	87.6	3176	6	AK030563	AK030563 Mus muscu
c	18	18	85.7	333	18	DU730974	DU730974 5F10_ENSD
c	19	18	85.7	646	15	AZ574416	AZ574416 328PvD11
c	20	18	85.7	746	11	EC607094	EC607094 Y70B12 YL
c	21	18	85.7	752	11	EC603953	EC603953 Y67D08 YL
	22	18	85.7	958	19	CNS02HZE	AL198275 Tetraodon
	23	18	85.7	1092	19	CNS05SXK	AL352433 Tetraodon
c	24	17.8	84.8	344	2	BF876167	BF876167 CM4-ET009
	25	17.8	84.8	453	2	BF876166	BF876166 CM4-ET009
	26	17.8	84.8	517	19	DE015081	DE015081 Branchios
c	27	17.8	84.8	541	2	BG864692	BG864692 602798388
	28	17.8	84.8	580	9	CK094803	CK094803 I055P43.3
c	29	17.8	84.8	597	3	BI124855	BI124855 I051P88P
c	30	17.8	84.8	620	9	CK104788	CK104788 I055P43.5
c	31	17.8	84.8	622	11	EE054461	EE054461 zf_30d3k_
c	32	17.8	84.8	625	3	BI125081	BI125081 I055P43P
c	33	17.8	84.8	748	15	AQ040360	AQ040360 CIT-HSP-2
c	34	17.8	84.8	800	9	CK477879	CK477879 AGENCOURT
c	35	17.8	84.8	821	18	CW996363	CW996363 OA_BBa007
c	36	17.8	84.8	849	9	CK310543	CK310543 SB02006B1
c	37	17.8	84.8	904	15	AQ787944	AQ787944 HS_3081_A
c	38	17.8	84.8	974	4	BQ944939	BQ944939 AGENCOURT
c	39	17.8	84.8	1299	12	DY301659	DY301659 KN0AAQ13Y
	40	17.8	84.8	1350	13	DN695090	DN695090 CGX98-A05
	41	17.4	82.9	253	3	BI382074	BI382074 BFLG2_000
	42	17.4	82.9	308	7	BB286061	BB286061 BB286061
	43	17.4	82.9	421	18	DX314559	DX314559 OR_ABa022
	44	17.4	82.9	438	5	BY382585	BY382585 BY382585
	45	17.4	82.9	494	16	CE014820	CE014820 tigr-gss-

ALIGNMENTS

RESULT 1
BI255229
LOCUS   BI255229   376 bp   mRNA   linear   EST 17-JUL-2001
DEFINITION   602978346F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123458 5',
             mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2732 Seconds
                                        (without alignments)
                                 545.032 Million cell updates/sec

Title: US-10-529-447-4
Perfect score: 24
Sequence: 1 tacacttgggtttcagtacgaggt 24

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:42:41 ; Search time 2504 Seconds
                                           (without alignments)
                                    545.032 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                          SUMMARIES
                    %
Result   Query

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 1214 Seconds
                                          (without alignments)
                                          1479.815 Million cell updates/sec

Title: US-10-529-447-24
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
       1   26 100.0   26 2   DD309755   DD309755 Method an
       2   26 100.0   26 2   DD309756   DD309756 Method an

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 1214 Seconds
                                           (without alignments)
                                           1479.815 Million cell updates/sec

Title: US-10-529-447-23·
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6:· gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No. Score Match Length DB   ID   Description
----
   1   26   100.0   26   2   DD309755   DD309755 Method an
   2   26   100.0   26   2   DD309756   DD309756 Method an

```
                        GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on:          July 16, 2007, 09:38:01 ; Search time 1074 Seconds
                                           (without alignments)
                                   1479.815 Million cell updates/sec


Title:          US-10-529-447-22
Perfect score:  23
Sequence:       1 ctccaacatgctatgcaacgtcc 23


Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0


Searched:       7568541 seqs, 34560148153 residues


Total number of hits satisfying chosen parameters:      15137082


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
                        %
Result              Query
   No.    Score   Match Length DB   ID                     Description
---------------------------------------------------------------------------
     1     23    100.0     23   2   DD309754               DD309754 Method an
c    2     23    100.0    450  10   DQ057302               DQ057302 Human pap
```

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 1028 Seconds
                                          (without alignments)
                                          1479.815 Million cell updates/sec

Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	2	DD309740	DD309740 Method an
c 2	22	100.0	7858	10	HPV45	X74479 Human papil

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 981 Seconds
                                          (without alignments)
                                          1479.815 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   21   100.0   21 2   DD309739   DD309739 Method an
c   2   21   100.0   23 2   AX742256   AX742256 Sequence

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 981 Seconds
                                           (without alignments)
                                 1479.815 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   21 100.0   21 2   DD309737   DD309737 Method an
     2   21 100.0   21 2   DD309738   DD309738 Method an

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 981 Seconds
                                          (without alignments)
                                          1479.815 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   21   100.0   21 2   DD309737   DD309737 Method an
    2   21   100.0   21 2   DD309738   DD309738 Method an

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 1121 Seconds
                                         (without alignments)
                                         1479.815 Million cell updates/sec

Title: US-10-529-447-4
Perfect score: 24
Sequence: 1 tacacttgggtttcagtacgaggt 24

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   24   100.0   24 2   DD309736   DD309736 Method an
  c 2   24   100.0   450 10 DQ057302   DQ057302 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:38:01 ; Search time 1028 Seconds
                                          (without alignments)
                                          1479.815 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   22 100.0   .22 2   DD309735   DD309735 Method an
     2   22 100.0   450 10 DQ057302   DQ057302 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 265 Seconds
                                    (without alignments)
                                    726.595 Million cell updates/sec

Title: US-10-529-447-24
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   26 100.0   26 12   ADM82971   Adm82971 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 265 Seconds
                                            (without alignments)
                                            726.595 Million cell updates/sec

Title: US-10-529-447-23
Perfect score: 26
Sequence: 1 agagacagcacaggcattgttccatg 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	26	12	ADM82971	Adm82971 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 235 Seconds
                                            (without alignments)
                                            726.595 Million cell updates/sec

Title: US-10-529-447-22
Perfect score: 23
Sequence: 1 ctccaacatgctatgcaacgtcc 23

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   23   100.0   23   12   ADM82970   Adm82970 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 224 Seconds
                                          (without alignments)
                                          726.595 Million cell updates/sec

Title: US-10-529-447-8
Perfect score: 22
Sequence: 1 caacacctgtgcatcattctga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                         %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
   1   22   100.0   22   12 ADM82958   Adm82958 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 214 Seconds
                                           (without alignments)
                                         726.595 Million cell updates/sec

Title: US-10-529-447-7
Perfect score: 21
Sequence: 1 acttgtgcatcattgtggacc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   21 100.0   21 12   ADM82957   Adm82957 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 214 Seconds
                                          (without alignments)
                                          726.595 Million cell updates/sec

Title: US-10-529-447-6
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score Match Length DB   ID   Description
----
    1   21   100.0   21 12   ADM82956   Adm82956 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 214 Seconds
                                    (without alignments)
                                    726.595 Million cell updates/sec

Title: US-10-529-447-5
Perfect score: 21
Sequence: 1 cattttgtgaacaggcagagc 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   21 100.0   21 12   ADM82956   Adm82956 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 245 Seconds
                                          (without alignments)
                                  726.595 Million cell updates/sec

Title: US-10-529-447-4
Perfect score: 24
Sequence: 1 tacacttgggtttcagtacgaggt 24

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
  No.   Score Match Length DB   ID   Description
----
   1   24   100.0   24   12 ADM82955   Adm82955 Human pap

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OM nucleic - nucleic search, using sw model

Run on: July 16, 2007, 09:16:44 ; Search time 224 Seconds
                                          (without alignments)
                                          726.595 Million cell updates/sec

Title: US-10-529-447-3
Perfect score: 22
Sequence: 1 acgattccacaacataggagga 22

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
    1   22   100.0   22   12 ADM82954   Adm82954 Human pap